

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant cell after pathogen infection, which plant nucleotide sequence is from a gene encoding a polypeptide that is substantially similar to a polypeptide encoded by a gene comprising a promoter selected from the group consisting of SEQ ID NOs: 1047, 1051, 1053, 4794, 4892, 5261, 5738 and 6469.
2. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant cell after pathogen infection, which plant nucleotide sequence hybridizes under high stringency conditions to the complement of any one of SEQ ID NOs: 1047, 1051, 1053, 4794, 4892, 5261, 5738 or 6469.
3. The isolated polynucleotide of claim 2, which plant nucleotide sequence hybridizes under very high stringency conditions to the complement of any one of SEQ ID NOs: 1047, 1051, 1053, 4794, 4892, 5261, 5738 or 6469.
4. The isolated polynucleotide of claim 1 or 2 which is selected from the group consisting of SEQ ID NOs: 1047, 1051, 1053, 4794, 4892, 5261, 5738, 6469, and a fragment thereof.
5. The polynucleotide of claim 1 or 2 wherein the plant nucleotide sequence is 25 to 2000 nucleotides in length.
6. The polynucleotide of claim 1 or 2 wherein the plant nucleotide sequence is from a dicot.

7. The polynucleotide of claim 1 or 2 wherein the plant nucleotide sequence is from a monocot.
8. The polynucleotide of claim 1 or 2 wherein the plant nucleotide sequence is from a cereal plant.
9. The polynucleotide of claim 1 or 2 wherein the plant nucleotide sequence is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat sequence.
10. An expression cassette comprising the polynucleotide of claim 1 or 2 operatively linked to an open reading frame.
11. A host cell comprising the expression cassette of claim 10.
12. The host cell of claim 11 wherein the cell is a yeast, a plant cell, a bacterium, a cereal plant cell, or an *Arabidopsis* cell.
13. The host cell of claim 11 which is a monocot cell.
14. The host cell of claim 11 which is a dicot cell.
15. A transformed plant, the genome of which is augmented with the expression cassette of claim 10.
16. The transformed plant of claim 15 which is a dicot.
17. The transformed plant of claim 15 which is a monocot.
18. The transformed plant of claim 15 which is selected from the group consisting of maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice, wheat and *Arabidopsis*.

19. A method for augmenting a plant genome, comprising:
- a) contacting a plant cell with an expression cassette comprising a promoter from a gene encoding a polypeptide that is substantially similar to a polypeptide encoded by a gene comprising a promoter selected from the group consisting of SEQ ID NOs: 1047, 1051, 1053, 4794, 4892, 5261, 5738 and 6469 operatively linked to an open reading frame so as to yield a transformed plant cell; and
 - b) regenerating the transformed plant cell to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the open reading frame in the cells of the plant.
20. A method to alter the phenotype of a plant cell comprising: introducing an expression cassette comprising a promoter from a gene encoding a polypeptide that is substantially similar to a polypeptide encoded by a gene comprising a promoter selected from the group consisting of SEQ ID NOs: 1047, 1051, 1053, 4794, 4892, 5261, 5738 and 6469 operatively linked to an open reading frame into the plant cell and expressing the open reading frame in the cell so as to alter a characteristic of that cell relative to a plant cell that does not comprise the expression cassette.
21. The method of claim 19 or 20 wherein the plant cell is a dicot cell.
22. The method of claim 19 or 20 wherein the plant is a monocot cell.
23. The method of claim 19 or 20 wherein the plant cell a cereal cell.
24. The method of claim 19 or 20 wherein the plant cell is selected from the group consisting of a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice, wheat and *Arabidopsis* cell.

25. The method of claim 19 or 20 wherein the open reading frame is in an antisense orientation relative to the nucleotide sequence which alters transcription.
26. The method of claim 19 or 20 wherein the expression inhibits transcription or translation of endogenous plant nucleic acid sequences corresponding to the open reading frame.
27. The method of claim 19 wherein the open reading frame is expressed in an amount that is greater than the amount in a plant which does not comprise the expression cassette.
28. The method of claim 18 or 19 wherein the open reading frame encodes a protein.
29. The method of claim 28 wherein the protein encodes a regulatory product.
30. The method of claim 28 wherein the expression of the open reading frame confers insect resistance, bacterial resistance, fungal resistance, viral resistance, or nematode resistance.
31. A transformed plant prepared by the method of claim 20 .
32. A product of the plant of claim 31 which comprises the expression cassette or the gene product encoded by the open reading frame.
33. The product of claim 32 which is selected from the group consisting of a seed, fruit, vegetable, transgenic plant, and a progeny plant.
34. A method to confer resistance or tolerance to a plant to a pathogen, comprising:
- a) contacting plant cells with an expression cassette comprising a polynucleotide encoding a polypeptide that is substantially similar to a

polypeptide encoded by an open reading frame comprising any one of SEQ ID NOs: 50, 139, 609, 4210, 3311, 3791, 2699, 3463, 3584, 4451 or 4595 so as to yield transformed cells; and

- b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the polynucleotide in the cells of the plant in an amount effective to confer resistance or tolerance to the plant to a pathogen relative to a corresponding plant which does not comprise the expression cassette.

35. The method of claim 34 wherein the cells are monocot cells.

36. The method of claim 34 wherein the cells are dicot cells.

37. The method of claim 34 wherein the open reading frame encodes a DNA binding protein, hormone response protein, membrane protein, metabolic protein, transposon, receptor/kinase, phosphatase, stress protein, cell wall protein, lipid transfer protein, heat shock protein, protein processing protein, RNA processing protein, non-cell wall structural protein or a non-kinase signaling protein.

38. A transformed plant prepared by the method of claim 34.

39. A seed of the plant of claim 38.

40. A progeny plant of the plant of claim 39.

41. A method to identify a plant cell infected with a pathogen, comprising:

- a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with at least one oligonucleotide under conditions effective to specifically amplify a nucleotide sequence corresponding to one

of SEQ ID NOs: 50, 139, 609, 4210, 3311, 3791, 2699, 3463, 3584, 4451 or 4595 or a portion thereof, so as to yield an amplified product; and

- b) detecting or determining the presence or amount of the amplified product, wherein the presence or amount of the amplified product is indicative of pathogen infection.

42. A method to identify a plant cell infected with a pathogen, comprising:

- a) contacting a sample comprising polypeptides obtained from a plant cell suspected of being infected with a pathogen with an agent that specifically binds to a polypeptide that is substantially similar to a polypeptide encoded by an open reading frame comprising one of SEQ ID NOs: 50, 139, 609, 4210, 3311, 3791, 2699, 3463, 3584, 4451 or 4595 so as to form a complex; and
- b) detecting or determining the presence or amount of the complex, wherein the presence or amount of the complex is indicative of pathogen infection.

43. A method to identify a plant cell infected with a pathogen, comprising:

- a) contacting nucleic acid obtained from a plant cell suspected of being infected with a pathogen with a probe corresponding to a sequence selected from the group consisting of SEQ ID Nos. 50, 139, 609, 4210, 3311, 3791, 2699, 3463, 3584, 4451 or 4595 or a portion thereof, under stringent hybridization conditions to form a duplex; and
- b) detecting or determining the presence or amount of the duplex, wherein the presence of a duplex is indicative of infection.